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Crystal Structure of C/EBP α bZIP Bound to DNA

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Beamline(s): X9B

Introduction: Basic region leucine zipper (bZIP) DNA-binding proteins are a large class of eukaryotic transcription factors. The members of the C/EBP (CCAAT/enhancer binding) family have been implicated in controlling a variety of cellular functions including cell differentiation, growth, and more recently tumorigenesis. To understand the molecular basis of their specific DNA recognition we have initiated crystallographic studies of complexes of several bZIP proteins with their cognate DNA oligomers.

Results: Cocrystals of C/EBP α bZIP peptide bound to 21-mer DNA were obtained in two crystal forms. Crystals best suitable for X-ray analysis belong to the P2₁2₁2 space group with a=140.89 Å, b=53.09 Å, c=67.41 Å. Diffraction data has been collected to 2.8 Å on a synchrotron source, at 100 K on beamline X9B. Structure has been solved by molecular replacement using the coordinates of CREB bZIP-DNA complex (PDB code: 1DH3 as a model). Refinement of the solution is in progress.